

DOCKET NO.: DIBIS-0002US.P3 (Counsel Docket No. 10450)**PATENT****In the Claims:**

The current status of all claims is listed below and supercedes all previous lists of claims.

1 – 22. (cancelled).

23. (currently amended) A method of identifying a virus comprising:

amplifying nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family to produce an amplification product; ~~wherein the amplification product corresponds to a bioagent identifying amplicon, and wherein the said conserved regions have at least 80% sequence identity among members of said viral family, which flank an intervening variable region; which exhibits no greater than 5% sequence identity among members of said viral family;~~

measuring the molecular mass of said amplification product by mass spectrometry;
and

comparing the molecular mass of said amplification product with four or more known molecular masses of ~~known bioagent identifying amplicons~~ amplification products of four or more members of said viral family produced by using said pair of primers wherein a match of molecular mass of said amplification product with a known molecular mass of a ~~known bioagent identifying amplicon~~ an amplification product of a member of said viral family indicates the identity of said virus.

24. (previously presented) The method of Claim 23, further comprising repeating said amplifying, measuring and comparing steps using one or more additional pairs of primers.

25. (previously presented) The method of Claim 23, wherein said virus is a biological warfare viral threat agent.

26. (previously presented) The method of claim 23, wherein said virus is identified at the sub-species level.

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27. (currently amended) The method of Claim 23, wherein said molecular mass of said amplification product is measured by electrospray ionization time-of-flight mass spectrometry.

28-29. (cancelled)

30. (currently amended) A method of identifying a virus comprising:

amplifying nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family to produce an amplification product, ~~wherein the amplification product corresponds to a bioagent identifying amplicon, and wherein the said conserved regions have at least 80% sequence identity among members of said viral family, which flank an intervening variable region; which exhibits no greater than 5% sequence identity among members of said viral family;~~

measuring the base composition of said amplification product; and

comparing the base composition of said amplification product with known base compositions of ~~known bioagent identifying amplicons~~ amplification products of members of said viral family produced by using said pair of primers wherein a match of base composition of said amplification product with a known base composition of a ~~known bioagent identifying amplicon~~ an amplification product of a member of said viral family indicates the identity of said virus.

31. (previously presented) The method of Claim 30, further comprising repeating said amplifying, measuring and comparing steps using one or more additional pairs of primers.

32. (previously presented) The method of Claim 30, wherein said virus is a biological warfare viral threat agent.

33. (previously presented) The method of Claim 30, wherein said virus is identified at the sub-species level.

34. (previously presented) The method of Claim 30, wherein said base composition of

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said amplification product is measured by mass spectrometry.

35-43. (cancelled)

44. (new) The method of claim 23 wherein said virus is a respiratory pathogen.

45. (new) The method of claim 23 wherein said virus is a hepatitis C virus.

46. (new) The method of claim 23 wherein said virus is an immunodeficiency virus.

47. (new) The method of claim 23 wherein said virus is a member of a viral family selected from the group consisting of *Filoviridae*, *Flaviviridae*, *Arenaviridae*, *Bunyaviridae*, *Adenoviridae*, *Picornaviridae*, *Togaviridae*, and *Coronaviridae*.

48. (new) The method of claim 23 wherein said housekeeping gene encodes a polymerase, a virion component, a helicase, a protease, a methyltransferase or an accessory protein.

49. (new) The method of claim 24 wherein said polymerase is RNA-dependent RNA polymerase, DNA-dependent DNA polymerase or DNA-dependent RNA polymerase.

50. (new) The method of claim 30 wherein said virus is a respiratory pathogen.

51. (new) The method of claim 30 wherein said virus is a hepatitis C virus.

52. (new) The method of claim 30 wherein said virus is an immunodeficiency virus.

53. (new) The method of claim 30 wherein said virus is a member of a viral family selected from the group consisting of *Filoviridae*, *Flaviviridae*, *Arenaviridae*, *Bunyaviridae*, *Adenoviridae*, *Picornaviridae*, *Togaviridae*, and *Coronaviridae*.

54. (new) The method of claim 30 wherein said housekeeping gene is a polymerase, a

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virion component, a helicase, a protease, a methyltransferase, or an accessory protein.

55. (new) The method of claim 54 wherein said polymerase is RNA-dependent RNA polymerase, DNA-dependent DNA polymerase or DNA-dependent RNA polymerase.